

Fig. 2 A



Fig. 2B

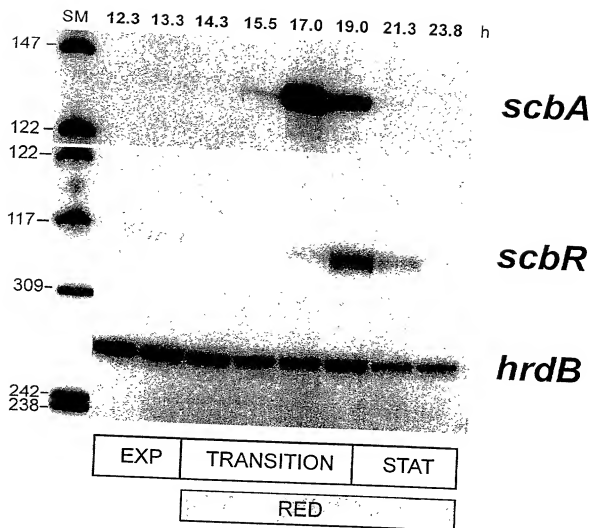


Fig. 3A

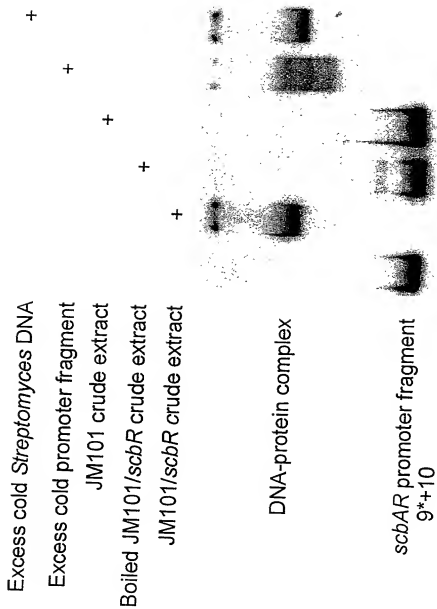


Fig. 38

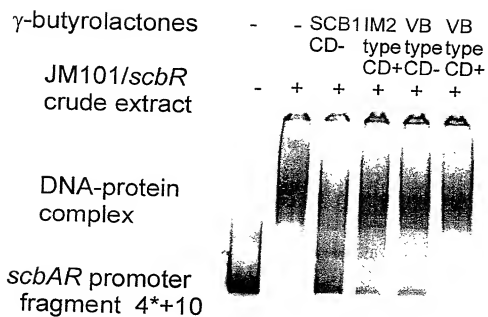


Fig. 4A

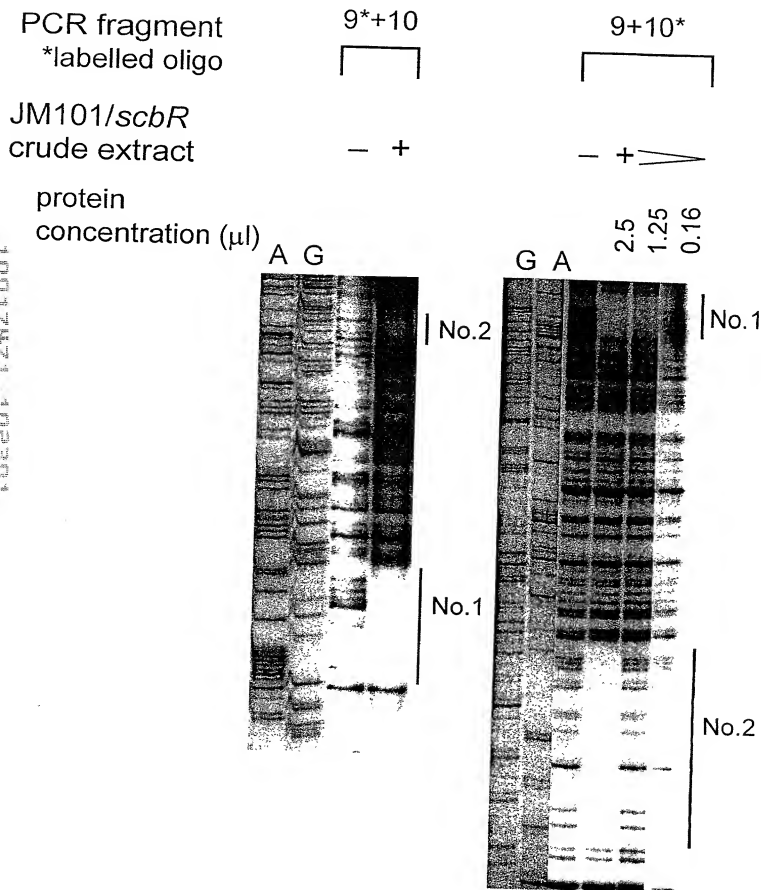


Fig. 48

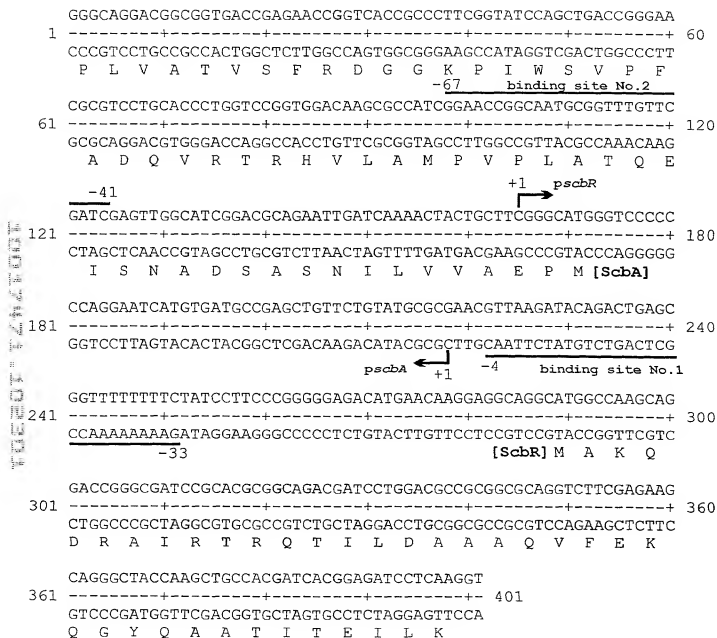


Fig. 5A

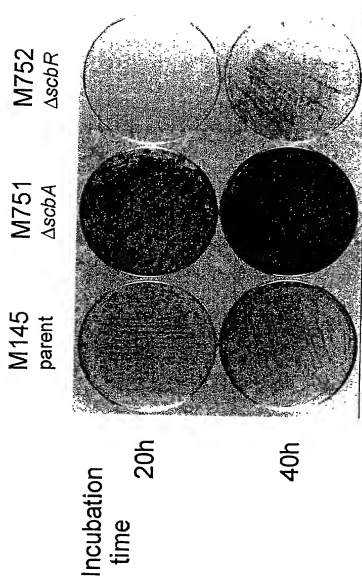




Fig. 58

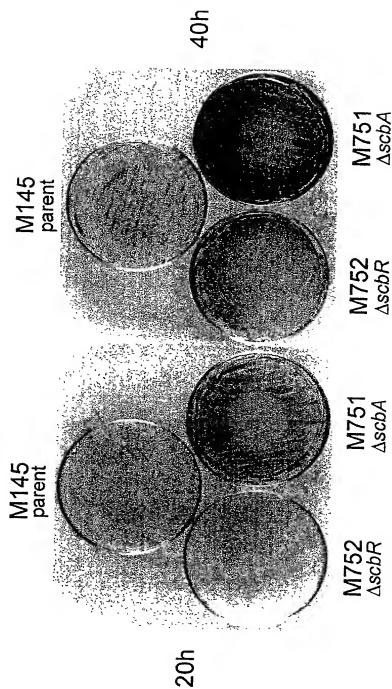
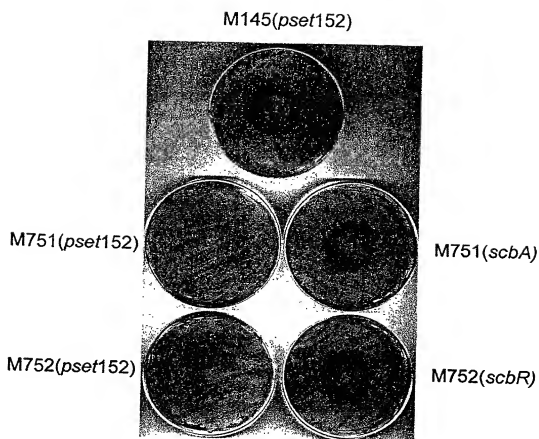
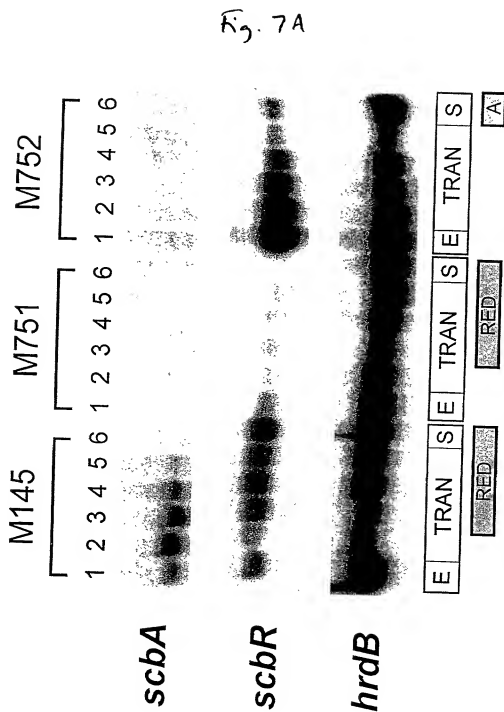


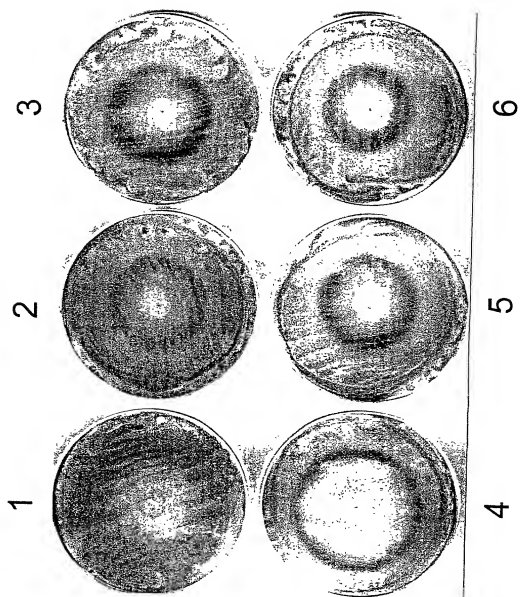
Fig. 6





Act production (ng/ml)	1) 12.0	3) 52	6) 200	1) 6.0	3) 250	6) 1844	1) 2.0	3) 6.0	6) 288
Red production (µg/ml)	1) 0.26	3) 0.44	6) 0.67	1) 0.06	3) 2.08	6) 6.40	1) 0	3) 0	6) 0.15

Fig. 7B



102201-12641001

Fig. 8

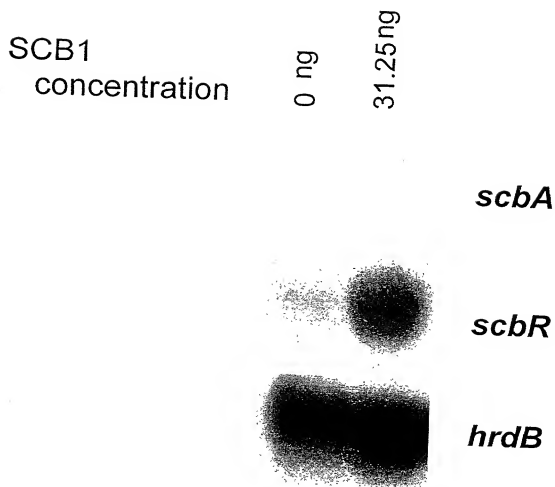


Fig. 9: ScbR amino acid sequence

MAKQDRAIRTRQTILDAAAQVFEKQGYQAATITEILKVAGVTKG  
ALYFHFQSKEELALGVFDAQEPPQAVPEQPPLRLQELIDMGMLFCHRLRTNVVARAGVR  
LSMDQQAHGLDRRGPFRRWHETLLKLLNQAKENGELLPHVVTDSADLYVGTFAGIQV  
VSQTVSDYQDLEHRYALLQKHILPAIAVPSVLAALDLSEERGARLAAELAPTGKD

Fig. 10: ScbA amino acid sequence

MPEAVVLINSASDANSIEQTALPVPMAIVHRTRVQDAFPVSWIP  
KGGDRFSVTAVLPHDHPFFAPVHGDRHDPLLIAETLRQAAMLVFHAGYGVFVGYHFLM  
TLDYTCHLDHLGVSGEVAEEVEVACSQLKFRGGQPVGQVWDVAVRRAGRLAATGTA  
TTRFTSPQVYRRMRGDFATPTASVPGTAPVPAARAGRTRDEDVVLSSASSQDQDWTWRLRV  
DTSHPTLFQRPNDHVPGMILLLEAARQAACLVTPAPFPVPSIGGTRFVRYAEFDSPCWI  
QATVRPGPAAGLTTRVVTGHQDGSIVFLTTLSGPAFSG

Fig. 11: ScbB amino acid sequence

MRAHGTRYGRPLEGKTALVTGSGRGIGRGIALRLAADGALVAVH  
YGSSEAAARETVETIRSSGGQALAIRAELGVVGDAALYAADFAGMGEFGVPPPEFDIL  
VNNAGVSGSGRITVEVTEVFDRLVAVNVRAPLFLVQHGLKRLRDGGRIINISSAATTR  
AFPESIGYAMTKGAVDTLTLALARQLGERGITVNAVAPGFVETDMNARRRQTPEAAAA  
LAAYSVFNRIGRPDDIADVVAFLASDDSRWITGQYVDATGGTIL

Fig. 12

# Act Production by *S.lividans* Strains Carrying

## pIJ68

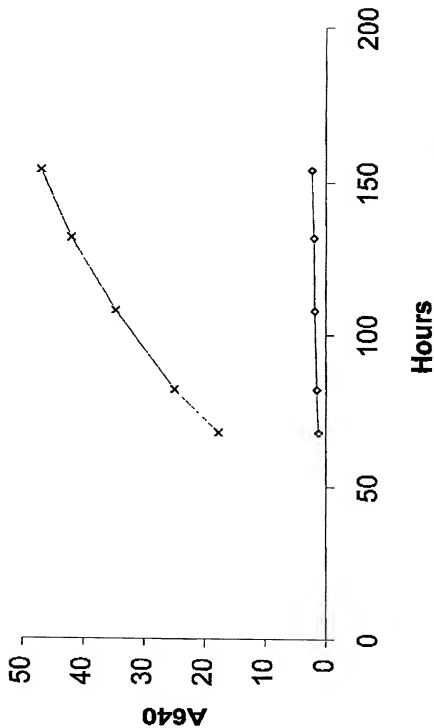


Fig. 13

# Red Production by *S. lividans* Strains Carrying pIJ6014

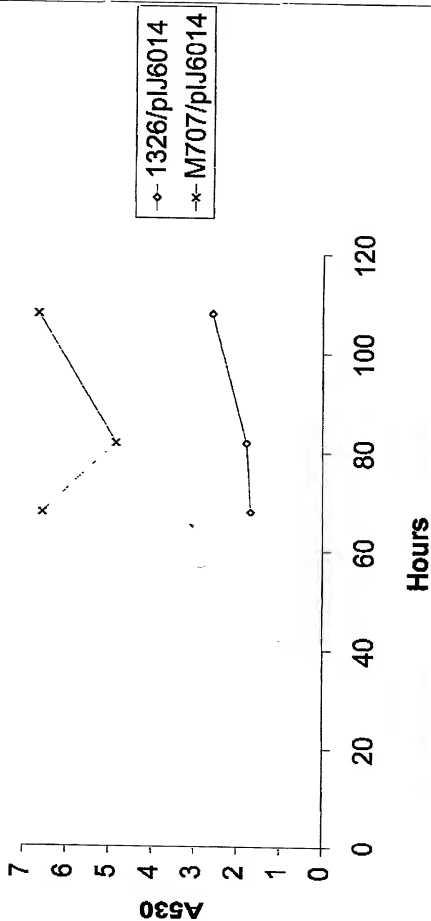




Fig. 14

DNA\_SEQUENCE Length: 4346kb..

1 **GTCTGAC**GACG GCGTCGGGTT CGACGCCGAC GCGGTACTCG TTCCCGGCCA  
*HincII*

51 CCGGGCACCG GGTCTGCGCT CGATGACCGA CCGCATCGAG GACGTCGGCT

101 GCGGGCTCCT GATAGTGAGC GGCCCCGCCG GCGGCACGCA CATCGACGTC

151 CATCTCCAC TGCGCCCCG GAAAGTGAGC ACCGCACCGC GGACGTGACG

201 CCATGGGAGG GCCACGTCCG CGGACGGATC ACCCCTGGCT TCGGCCGAAG

251 GCTTCCGCGT GGTCCGCCG CCAGATGCGG AACGGCTGG CGGGCCGGCC

301 CGTCACTTCC CGCACGGTCG GCACGACCTG CGCCTTGGCC CCCGCCCGCT

351 GCCGCTCGGC GCTCTCAGG AACCGTCGCG CGACGGGCTT CGGATACTTC

401 CGGAGCATCT GCTCGCGCGC CGCCTCCAGC CCCAGTCTCT CGAAACGCAG

451 TGACCGCCCC AGCACCTCGG AGAGCCGCGC CGTCTGCTGC CTGGCGGTGA

501 TCGCCTCGGG CCCGGACAGC GCGTACGCCC GTCCCTCGTG GCCGGGCCGG

551 GTCAGTGCCC TGACCGCCAC TTCCGCGATG TCGCGCGGAT CGACGCAGGC

601 AACCGGGGAC GTGCCGTACA GCGCGCGGAC CACGCCGTCG GACCGGATGG

651 CGGGCGCCCA GGACAGCGTG TTGGACATGA AGGTCCTGGC CCGCAGGAAG

701 GTCCAGTCTA GCCCGGACTC GCGTACGGCC CGTCTGTTCT CGCGCTGCCG

751 CCGCGTGATG AAGTCGTCCG CGCCCGGTTT CCCCACCGCG AGCATGGACA

801 GCTTCACCAG GTGCCGGACG CCGGCCTCGC GCGCCGCCG CGCGAAACGC

851 TCGTCGTCCG GCTCGGTGGC ACTGTTCTGT ACGAGGAACG CCGCCCGCAC

901 CCCGTTGAGG GCCCGGTCCA GGCCCGGGCG GTCGCGGTAC TCGCCCGCGC

951 AGACCTCGAC GTTCGGGCGG GTGACGCTCA CCCGTTCCGG CCGCCGGGCG

1001 AGGACTCTGA CGGGACCGGT CCGGGCCAGC AGGTGGGCGA CCTGACGGCC

1051 GACCACACCG GTCACGCCGG TCACAAGAAT CACTCGGGGC TCCTCTCGGG

1101 CAGCGAGGCA GGGGCGCCTC CGaacAtACA TATGAGGGGA Agggcaggat

1151 ctgccccggg ggcggaaccg gcgatgttcg cgccccGGG CCGGTGCTTC

1201 AGCCGAGAA CGCGGGGCGG GACAGCGTGG TGAGGAAGAC GAGGCTGCCG

1251 TCCTGATGCC CGGTGACCG CACGGTGGTC AGCCCCGCCG CCGGCCCCGG

1301 CCGGACCGTC GCCT**GGATC/C** AGCACGGGCT GTCGAACCTC GCGTACCGGA  
*BamHI*

1351 CGAACCGGGT GCCGCCGATC GACGGCACGA AGGGCGCCGG ACCGGTCACG  
 1401 AGGCACGCGG CCTGCCGTGC CGCCTCGAGC AGCAGCATGC CCGGTACGTG  
 1451 GTCGTTGGGG CGCTGGAAGA GGGTCGGGTG ACTGGTGTCC ACCCGCAGTC  
 1501 GCCACGTGTC CTGCTGCGAA CTCGCCGACA GGACCACGTC CTCGTCGCGG  
 1551 GTGCGACCGG CGCGCGCCGC GGGCACGGGC GCGGTCCC GGACCGATGC  
 1601 GGTGGGAGTC GCGAAGTCGC CGCGCATCCG CCGGTAGACT TGAGGACTGG  
 1651 TGAAGCGCGT CGTGGCAGTC CCCGTGGCAG CGAGCCGTCC GGC GCGGCGC  
 1701 ACGGCCAGT CCACCTGTCC CTGTACGGGC TGCCCGCCGC GGAACCTCAG  
 1751 CTGGGAACAG GCCACTTCCA CCTCCAGCTC CGCGACCTCG CCCGACACGC  
 1801 CGAGGTGGTC GAGGTGGCAG GTGTAGTCCA GCGTGGCCAT CAGGAAGTGG  
 1851 TAGCCCACCG GCACGCCGTA GCCGGCGTGG AAGACGAGCA TCGCCGCTG  
 1901 ACGCAGGGTC TCGGCGATCA GCAGCGGATC GTGTCGGTCC CCGTGGACCG  
 1951 GTGCGAAGAA CGGGTGGTCG TGGGGCAGGA CGGCGGTGAC CGAGAACC GG  
 2001 TCACCGCCCT TCGGTATCCA **G/CTG**ACCGGG AACCGTCCT GCACCCTGGT

*PvuII*

2051 CCGGTGGACA AGCGCCATCG GAACCGGCAA TGCGGTTTGT TCGATCGAGT  
 2101 TGGCATCGGA CGCAGAATTG ATCAAACTA CTGCTTCGGG CATGGGTCCC  
 2151 CCCAGGAAT CATGTGATGC CGAGCTGTTC TGTATGCGCG AACGTTAAGA  
 2201 TACAGACTGA GCGGTTTTTT TTCTATCCTT CCCGGGGGAG ACATGAACAA  
 2251 GGAGGCAGGC ATGGCCAAGC AGGACCGGGC GATCCGCACG CGGCAGACGA  
 2301 TCCTGGACGC CGCGGCGCAG GTCTTCGAGA AGCAGGGCTA CCAAGCTGCC  
 2351 ACGATCACG/G AGATCCTCAA GGTGGCCGGG GTGACCAAGG GAGCCCTCTA

**CTGCA/GATG** designed primer to generate *PstI* site

*PstI*

2401 CTTCCTTTC CAGTCCAAGG AAGAACTGGC GCTGGGCGTC TCGACGCC  
 2451 AGGAACCACC ACAGGCCGTT CCGGAGCAAC CCCTCCGGCT GCAAGAAGTC  
 2501 ATCGACATGG GCATGTTGTT CTGTCACCGC TTGCGCACGA ACGTCGTGGC  
 2551 CCGGGCCGGC GTGCGCCTCT CCATGGACCA GCAGGCGCAC GGTCTCGATC  
 2601 GCCGAGGACC CTTCCGTCGC TGGCACGAGA CACTCCTGAA GCTGCTGAAC  
 2651 CAGGCAAGG AGAACGGTGA GTTGCTGCCC CATGTGGTCA CCACCGACTC  
 2701 GGCGATCTC TACGTGGGCA CGTTCGCCGG GATACAGGTC GTGTCCAGA  
 2751 CGGTGAGCGA CTACCAGGAC CTCGAACACC GCTACGCGCT **GCTGCA/GAAG**

*PstI*

2801 CACATCCTGC CCGCCATCGC GGTTCCTTCC GTGCTGGCCG CGCTCGATCT  
 2851 CTCCGAGGAG CGCGGAGCAC GCCTCGCGGC CGAACTGGCA CCGACCGGA  
 2901 AGGACTGACC GCCGAAGCGC CCGCACCGGA TACCGACCGC CCGTGCCCGA  
 2951 GCGGCCGACC GGGGCCGCCT ACGGGCCCGG CGGCGGGCCC GTAGGTCTGC  
 3001 CCTGCGTACC GAAGCGTGGC GGGTCAGAGA ATCGTTCCGC CTGTGGCATC  
 3051 GACGTACTGG CCGGTGATCC ACCGTGAGTC GTCGGAGGCC AGAAAGGCCA  
 3101 CCACGTCGGC GATGTCGTCG GGTCTGCCGA TCGGTTGAA CACGGAGTTG  
 3151 GCGGCCAGTG CCGCGGCCGC CTCGGGGGTC TGCCGCCGCC GTGCGTTCAT  
 3201 GTCCGTCTCC ACGAAACCCG GCGCCACCGC GTTGACCGTG ATCCCCGTT  
 3251 CCCCAGTTG CCTGGCCAGG GCGAGCGTGA GCGTGCCAC CGCACCTTG  
 3301 GTCATCGCGT ATCCGATGGA CTCGGGAAC GCGCGCCGGG TCGCGGCAGA  
 3351 CGAGATGTTG ATGATCCGCC CGCCGTCGCG CAGTCGTTT AGTCCGTGCT  
 3401 GGACCAGGAA CAGCGGTGCC CGGAC**GTGA** CGGCGACCAG TCGGTCGAAG

*HincII*

3451 ACCTCCTCGG TGA**CTT**CCGT GATCCGTCCC GAGCCGCTGA CGCCCGCGTT  
 3501 GTTCA**CC**AGG ATGTCGA**ACT** CGGGCGGCAC TCCGA**ACT**CG CCCATCCCGG  
 3551 CGTCGAACGC CGCGTAGAGC GCGGCCGCGT CACCCACGAC GCCGAGTTCG  
 3601 GCCCGGATGG CCAACGCCTG TCCGCCGCTG CTCCGGATGG TCTCGACGGT  
 3651 CTCTCGCGCC GCGGCCTCGC TGCTGCCGTA GTGGACTGCC ACGAGCGCCC  
 3701 CGTCCGCGGC CAGCCCGAGG GCGATACCGC GTCGATGCC CCGGCTTCCC  
 3751 CCGGTACCA GGGCGGTCTT GCCCTCCAGC GGTCTTCCAT ACCTCGTCCC  
 3801 ATGTGCACGC ATATCAGCCC CCGCCGTGCG TGAGCGACCC ATGGCGGCCG  
 3851 CTCGGCCGTT CGAATCGACG GTCACAGCCT ACCTGTGACC GCGTCAGACG  
 3901 GGGCCGGAGT GGCCCGGTTG GACGGCTGGG GCCAGATCGG GCGGCGCGCA  
 3951 CGGGGAACCG GCGCCGGTCA GGGGT**CAGGG** GTCGCCGGGA CCGCCAGGC  
 4001 CGGTCAGGGC ACCGACCGGA TCGAGGTCGG GCGTGCCACG CGGCCACCAG  
 4051 TCCTCGCGGC CCAGCTCCGA CTCGTACGCG TACCAGAGCC CCGTCCGGCC  
 4101 GAGTCTGAGC TGGACGTGGC CGCGCGGGTG GGTGAGGCGG TTGCGCCAGG  
 4151 GCGGAAGGC GGGGAGGTCG GCGCGAGCA TCATGGGCGG GCGCGGTGCG  
 4201 AAACGGCCGG CCGCGGGGTC CCAGGGCTCC TCCAGGACGT CTAGACCCGC  
 4251 CAACCCGCCG TGCCGCCAGG CGGCGACGGC CCGCGCCAGC TCCCGCGTGT  
 4301 CGCGTCCGGC GGCCGAGGCG AGCGACGCGT AGAGCGCGCG **GGTACC**

*KpnI*